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RAW SEQUENCE LISTING DATE: 10/17/2001
PATENT APPLICATION: US/09/924,338 TIME: 15:39:53

Input Set : N:\Crf3\RULE60\09924338.txt
Output Set: N:\CRF3\10172001\I924338.raw

SEQUENCE LISTING

(1) GENERAL INFORMATION:
(i) APPLICANT: Tobin, James
(ii) TITLE OF INVENTION: HUMAN INTERLUEKIN-11 RECEPTOR
(iii) NUMBER OF SEQUENCES: 4
(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Genetics Institute, Inc.
(B) STREET: 87 CambridgePark Drive
(C) CITY: Cambridge
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02140

ENTERED

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
(vi) CURRENT APPLICATION DATA:
C--> **(A) APPLICATION NUMBER: US/09/924,338**
C--> **(B) FILING DATE: 07-Aug-2001**
(C) CLASSIFICATION:
(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 09/151,102
(B) FILING DATE: 1998-09-10
(A) APPLICATION NUMBER: 08/362,304
(B) FILING DATE: 22-DEC-1994
(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Brown, Scott A.
(B) REGISTRATION NUMBER: 32,724
(C) REFERENCE/DOCKET NUMBER: GI5252
(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (617) 498-8224
(B) TELEFAX: (617) 876-5851
(2) INFORMATION FOR SEQ ID NO: 1:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2456 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 734..1999
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TCGCCCACCC CCAGCCTCTG GCAGCAGCCA GGGCATCTGG ATCTGCTTAA CTACACAGCC 60
CCAGCCTGCA CCCTAGCCCC ATCCAGCTTC ACAAACTGGA GACCAACGAA GTGTCAAGAG 120

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72 CCAGGCCCAG CTGAGTGGCC CAAGTAGCCA GACCAAGGAG CCAGGTTCAG GCGAGAAGCC     180
74 TGGCAGCCAG GGCAGGGGTG GGCCTCAGGG TGGGAGTGCA GGATGGGCTC AGATCCATGA     240
76 TGACACCCTT CCCCCAGGGT GATAAGGTCT GCCTAGGTTA ATCAGAGGCA GTGATAAGCC     300
78 CTGGACCAGG TGGGGGTAAA TACCAGAATT CCCAACAGCT GGACTGGAGG GGTTAATGGG     360
80 AGTGGCTGAG CTGGTGCCAG TGCTTGGTGC CAGGGGTGGG CGCCAAGGGC AGTGGAGGGG     420
82 GAGTTGCTGG CACAGTCTGT TGCCTCCGGC TTTTGTTCTG GGCCCTAAGC CCAGGACTGA     480
84 GATGGAGGGT GTGAGGGGGT GTGTGTGTCC GTGTGTGTGT GTGTGTGTGT GTGCGCGCGC     540
86 ACGCACATGC AAAGCACTGG GTATACAGTG GGAAAGGGGA CCTCAGGTCA GTTCCCGCAG     600
88 TGATTTCTAA CAGCCTTACC CCACTTGGTG CATCAATTTT TCTCCTAGGA AGCCTCAGTT     660
90 TTGGAGAGGA AGAGCCAGGC TTTAGCCTCC CATCTCAGGG GTCGGGGATT TTTGACTCTA     720
92 CCTCTCCCCA CAG ATG AGC AGC AGC TGC TCA GGG CTG AGC AGG GTC CTG         769
93                 Met Ser Ser Ser Cys Ser Gly Leu Ser Arg Val Leu
94                   1               5                  10
96 GTG GCC GTG GCT ACA GCC CTG GTG TCT GCC TCC TCC CCC TGC CCC CAG       817
97 Val Ala Val Ala Thr Ala Leu Val Ser Ala Ser Ser Pro Cys Pro Gln
98           15                  20                  25
100 GCC TGG GGC CCC CCA GGG GTC CAG TAT GGG CAG CCA GGC AGG TCC GTG       865
101 Ala Trp Gly Pro Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Ser Val
102      30                  35                  40
104 AAG CTG TGT TGT CCT GGA GTG ACT GCC GGG GAC CCA GTG TCC TGG TTT       913
105 Lys Leu Cys Cys Pro Gly Val Thr Ala Gly Asp Pro Val Ser Trp Phe
106  45                  50                  55                  60
108 CGG GAT GGG GAG CCA AAG CTG CTC CAG GGA CCT GAC TCT GGG CTA GGG       961
109 Arg Asp Gly Glu Pro Lys Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly
110                  65                  70                  75
113 CAT GAA CTG GTC CTG GCC CAG GCA GAC AGC ACT GAT GAG GGC ACC TAC      1009
114 His Glu Leu Val Leu Ala Gln Ala Asp Ser Thr Asp Glu Gly Thr Tyr
115              80                  85                  90
117 ATC TGC CAG ACC CTG GAT GGT GCA CTT GGG GGC ACA GTG ACC CTG CAG      1057
118 Ile Cys Gln Thr Leu Asp Gly Ala Leu Gly Gly Thr Val Thr Leu Gln
119          95                 100                 105
121 CTG GGC TAC CCT CCA GCC CGC CCT GTT GTC TCC TGC CAA GCA GCC GAC      1105
122 Leu Gly Tyr Pro Pro Ala Arg Pro Val Val Ser Cys Gln Ala Ala Asp
123     110                 115                 120
125 TAT GAG AAC TTC TCT TGC ACT TGG AGT CCC AGC CAG ATC AGC GGT TTA      1153
126 Tyr Glu Asn Phe Ser Cys Thr Trp Ser Pro Ser Gln Ile Ser Gly Leu
127 125                 130                 135                 140
129 CCC ACC CGC TAC CTC ACC TCC TAC AGG AAG AAG ACA GTC CTA GGA GCT      1201
130 Pro Thr Arg Tyr Leu Thr Ser Tyr Arg Lys Lys Thr Val Leu Gly Ala
131                 145                 150                 155
133 GAT AGC CAG AGG AGG AGT CCA TCC ACA GGG CCC TGG CCA TGC CCA CAG      1249
134 Asp Ser Gln Arg Arg Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln
135             160                 165                 170
137 GAT CCC CTA GGG GCT GCC CGC TGT GTT GTC CAC GGG GCT GAG TTC TGG      1297
138 Asp Pro Leu Gly Ala Ala Arg Cys Val Val His Gly Ala Glu Phe Trp
139         175                 180                 185
141 AGC CAG TAC CGG ATT AAT GTG ACT GAG GTG AAC CCA CTG GGT GCC AGC      1345
142 Ser Gln Tyr Arg Ile Asn Val Thr Glu Val Asn Pro Leu Gly Ala Ser
143     190                 195                 200
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```
145 ACA CGC CTG CTG GAT GTG AGC TTG CAG AGC ATC TTG CGC CCT GAC CCA      1393
146 Thr Arg Leu Leu Asp Val Ser Leu Gln Ser Ile Leu Arg Pro Asp Pro
147 205                 210                 215                 220
149 CCC CAG GGC CTG CGG GTA GAG TCA GTA CCA GGT TAC CCC CGA CGC CTG      1441
150 Pro Gln Gly Leu Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Arg Leu
151                 225                 230                 235
153 CGA GCC AGC TGG ACA TAC CCT GCC TCC TGG CCG TGC CAG CCC CAC TTC      1489
154 Arg Ala Ser Trp Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe
155             240                 245                 250
157 CTG CTC AAG TTC CGT TTG CAG TAC CGT CCG GCG CAG CAT CCA GCC TGG      1537
158 Leu Leu Lys Phe Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp
159         255                 260                 265
161 TCC ACG GTG GAG CCA GCT GGA CTG GAG GAG GTG ATC ACA GAT GCT GTG      1585
162 Ser Thr Val Glu Pro Ala Gly Leu Glu Glu Val Ile Thr Asp Ala Val
163     270                 275                 280
165 GCT GGG CTG CCC CAT GCT GTA CGA GTC AGT GCC CGG GAC TTT CTA GAT      1633
166 Ala Gly Leu Pro His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp
167 285                 290                 295                 300
169 GCT GGC ACC TGG AGC ACC TGG AGC CCG GAG GCC TGG GGA ACT CCG AGC      1681
170 Ala Gly Thr Trp Ser Thr Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser
171                 305                 310                 315
173 ACT GGG ACC ATA CCA AAG GAG ATA CCA GCA TGG GGC CAG CTA CAC ACG      1729
174 Thr Gly Thr Ile Pro Lys Glu Ile Pro Ala Trp Gly Gln Leu His Thr
175             320                 325                 330
177 CAG CCA GAG GTG GAG CCT CAG GTG GAC AGC CCT GCT CCT CCA AGG CCC      1777
178 Gln Pro Glu Val Glu Pro Gln Val Asp Ser Pro Ala Pro Pro Arg Pro
179         335                 340                 345
181 TCC CTC CAA CCA CAC CCT CGG CTA CTT GAT CAC AGG GAC TCT GTG GAG      1825
182 Ser Leu Gln Pro His Pro Arg Leu Leu Asp His Arg Asp Ser Val Glu
183     350                 355                 360
185 CAG GTA GCT GTG CTG GCG TCT TTG GGA ATC CTT TCT TTC CTG GGA CTG      1873
186 Gln Val Ala Val Leu Ala Ser Leu Gly Ile Leu Ser Phe Leu Gly Leu
187 365                 370                 375                 380
189 GTG GCT GGG GCC CTG GCA CTG GGG CTC TGG CTG AGG CTG AGA CGG GGT      1921
190 Val Ala Gly Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Gly
191                 385                 390                 395
193 GGG AAG GAT GGA TCC CCA AAG CCT GGG TTC TTG GCC TCA GTG ATT CCA      1969
194 Gly Lys Asp Gly Ser Pro Lys Pro Gly Phe Leu Ala Ser Val Ile Pro
195             400                 405                 410
197 GTG GAC AGG CGT CCA GGA GCT CCA AAC CTG TAGAGGACCC AGGAGGGCTT       2019
198 Val Asp Arg Arg Pro Gly Ala Pro Asn Leu
199         415                 420
201 CGGCAGATTC CACCTATAAT TCTGTCTTGC TGGTGTGGAT GGATGGACAG ATAGAAACCA    2079
203 GGCAGGACAG TAGATCCCTA TGGTTGGATC TCAGCTGGAA GTTCTGTTTG GAGCCCATTT    2139
205 CTGTGAGACC CTGTATTTCA AATTTGCAGC TGAAAGGTGC TTGTACCTCT GATTTCACCC    2199
207 CAGAGTTGGA GTTCTGCTCA AGGAACGTGT GTAATGTGTA CATCTGTGTC CATGTGTGAC    2259
209 CATGTGTCTG TGAGGCAGGG AACATGTATT CTCTGCATGC ATGTATGTAG GTGCCTGGGG    2319
211 AGTGTGTGTG GGTCCTTGGC TCTTGGCCTT TCCCCTTGCA GGGGTTGTGC AGGTGTGAAT    2379
213 AAAGAGAATA AGGAAGTTCT TGGAGATTAT ACTCAGAAAA AAAAAAAAAA AGTCGACGCG    2439
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GCCGCGAATT CCTGCAG 2456

(2) INFORMATION FOR SEQ ID NO: 2:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 422 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Met Ser Ser Ser Cys Ser Gly Leu Ser Arg Val Leu Val Ala Val Ala
 1               5                  10                  15
Thr Ala Leu Val Ser Ala Ser Ser Pro Cys Pro Gln Ala Trp Gly Pro
            20                  25                  30
Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Ser Val Lys Leu Cys Cys
        35                  40                  45
Pro Gly Val Thr Ala Gly Asp Pro Val Ser Trp Phe Arg Asp Gly Glu
    50                  55                  60
Pro Lys Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Glu Leu Val
65                  70                  75                  80
Leu Ala Gln Ala Asp Ser Thr Asp Glu Gly Thr Tyr Ile Cys Gln Thr
                85                  90                  95
Leu Asp Gly Ala Leu Gly Gly Thr Val Thr Leu Gln Leu Gly Tyr Pro
            100                 105                 110
Pro Ala Arg Pro Val Val Ser Cys Gln Ala Ala Asp Tyr Glu Asn Phe
        115                 120                 125
Ser Cys Thr Trp Ser Pro Ser Gln Ile Ser Gly Leu Pro Thr Arg Tyr
    130                 135                 140
Leu Thr Ser Tyr Arg Lys Lys Thr Val Leu Gly Ala Asp Ser Gln Arg
145                 150                 155                 160
Arg Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Gly
                165                 170                 175
Ala Ala Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Gln Tyr Arg
            180                 185                 190
Ile Asn Val Thr Glu Val Asn Pro Leu Gly Ala Ser Thr Arg Leu Leu
        195                 200                 205
Asp Val Ser Leu Gln Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly Leu
    210                 215                 220
Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Arg Leu Arg Ala Ser Trp
225                 230                 235                 240
Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe Leu Leu Lys Phe
                245                 250                 255
Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp Ser Thr Val Glu
            260                 265                 270
Pro Ala Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala Gly Leu Pro
        275                 280                 285
His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala Gly Thr Trp
    290                 295                 300
Ser Thr Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly Thr Ile
305                 310                 315                 320
Pro Lys Glu Ile Pro Ala Trp Gly Gln Leu His Thr Gln Pro Glu Val
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```
                325                 330                 335
Glu Pro Gln Val Asp Ser Pro Ala Pro Pro Arg Pro Ser Leu Gln Pro
            340                 345                 350
His Pro Arg Leu Leu Asp His Arg Asp Ser Val Glu Gln Val Ala Val
        355                 360                 365
Leu Ala Ser Leu Gly Ile Leu Ser Phe Leu Gly Leu Val Ala Gly Ala
    370                 375                 380
Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Gly Gly Lys Asp Gly
385                 390                 395                 400
Ser Pro Lys Pro Gly Phe Leu Ala Ser Val Ile Pro Val Asp Arg Arg
                405                 410                 415
Pro Gly Ala Pro Asn Leu
            420
(2) INFORMATION FOR SEQ ID NO: 3:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1714 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: cDNA
   (iii) HYPOTHETICAL: NO
    (ix) FEATURE:
          (A) NAME/KEY: CDS
          (B) LOCATION: 34..1359
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
TTCTTAGCCT GATAGGAGGA AGTCTTGGAG GCC ATG GCA CTC AGT CAC TGT GAT       54
                                    Met Ala Leu Ser His Cys Asp
                                      1               5
TAT CAA GAT GAG CAG CAG CTG CTC AGG GCT GAC CAG GGT CCT GGT GGC      102
Tyr Gln Asp Glu Gln Gln Leu Leu Arg Ala Asp Gln Gly Pro Gly Gly
         10                  15                  20
CGT GCT ACA GCC CTG GTG TCT TCC TCC TCC CCC TGC CCC CAA GCT TGG      150
Arg Ala Thr Ala Leu Val Ser Ser Ser Ser Pro Cys Pro Gln Ala Trp
     25                  30                  35
GGT CCT CCA GGG GTC CAG TAT GGA CAA CCT GGC AGG CCC GTG ATG CTG      198
Gly Pro Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Pro Val Met Leu
 40                  45                  50                  55
TGC TGC CCC GGA GTG AGT GCT GGG ACT CCA GTG TCC TGG TTT CGG GAT      246
Cys Cys Pro Gly Val Ser Ala Gly Thr Pro Val Ser Trp Phe Arg Asp
                 60                  65                  70
GGA GAT TCA AGG CTG CTC CAG GGA CCT GAC TCT GGG TTA GGA CAC AGA      294
Gly Asp Ser Arg Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Arg
             75                  80                  85
CTG GTC TTG GCC CAG GTG GAC AGC CCT GAT GAA GGC ACT TAT GTC TGC      342
Leu Val Leu Ala Gln Val Asp Ser Pro Asp Glu Gly Thr Tyr Val Cys
         90                  95                 100
CAG ACC CTG GAT GGT GTA TCA GGG GGC ATG GTG ACC CTG AAG CTG GGC      390
Gln Thr Leu Asp Gly Val Ser Gly Gly Met Val Thr Leu Lys Leu Gly
     105                 110                 115
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VERIFICATION SUMMARY DATE: 10/17/2001
PATENT APPLICATION: US/09/924,338 TIME: 15:39:54

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Output Set: N:\CRF3\10172001\I924338.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]